

- AD  
Contd
- complexation agents; and
- c) means for quantifying ratios of said metabolites to provide corresponding phenotypic determinants;

wherein said phenotypic determinants provide a metabolic phenotype profile of said individual and said steps b) and/or c) are effected according to the method of claim 6.

#### REMARKS

Table 4 is amended to correct two typographical errors. The probe substrate for CYP2C9 should read s-ibuprofen, not Diclofenac. Support for this amendment is found in the Specification on page 89, lines 24-27. The probe substrate for CYP2C19 should read Mephenytoin, not s-ibuprofen. Support for this amendment is found in the Specification on page 85, lines 25-28. Claim 46 is amended to clarify the claim by deleting dependence on Claim 44 and to correct a typographic error in the spelling of "phenotypic". Support for this amendment is found, for example, in originally-filed Claims 44 and 46. No new matter has been added.

#### CONCLUSION

In view of the above amendments and remarks, it is believed that all claims are in condition for allowance, and it is respectfully requested that the application be passed to issue. If the Examiner feels that a telephone conference would expedite prosecution of this case, the Examiner is invited to call the undersigned at (978) 341-0036.

Respectfully submitted,

HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

By Deirdre E. Sanders

Deirdre E. Sanders

Registration No. 42,122

Telephone: (978) 341-0036

Facsimile: (978) 341-0136

Concord, MA 01742-9133

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MARKED UP VERSION OF AMENDMENTS

Specification Amendments Under 37 C.F.R. § 1.121(b)(1)(iii)

Replace Table 4 at page 135, with the below Table marked up by way of bracketing and underlining to show the changes relative to the previous version of the Table.

**Table 4**  
**Examples of Enzymes and Corresponding Probes Drugs**

<b>Enzyme</b>	<b>Probe substrate</b>
NAT1	p-aminosalicylic acid
NAT2	Caffeine
CYP1A2	Caffeine
CYP2A6	Coumarin
CYP2C9	[Diclofenac] <u>s-ibuprofen</u>
CYP2C19	[s-ibuprofen] <u>Mephenytoin</u>
CYP2D6	Dextromethorphan
CYP2E1	Chlorzoxazone
CYP3A4	Midazolam

Claim Amendments Under 37 C.F.R. § 1.121(c)(1)(ii)

46. [The assay system of claim 44 comprising:](Amended) An assay system for detecting the presence of multiple determinant-specific metabolites in a biological sample obtained from an individual treated with at least one probe substrate specific for metabolic pathways of said metabolites, said system comprising:
- a) means for receiving said biological sample, including a plurality of affinity complexation agents contained therein;
  - b) means for detecting presence of said metabolites bound to said affinity complexation agents; and

- c) means for quantifying ratios of said metabolites to provide corresponding  
[pheontypic] phenotypic determinants;

wherein said phenotypic determinants provide a metabolic phenotype profile of said individual  
and said steps b) and/or c) are effected according to the method of claim 6.